



SEQUENCE LISTING

<110> HOFSTEENGE; Jan  
KEUSCH; Jeremy

<120> ASSAYS FOR C-MANNOSYLTRANSFERASE

<130> 1-32709A/FMI

<140> 10/530,457

<141> 2005-04-15

<150> PCT/EP03/011139

<151> 2003-10-08

<150> GB0223449

<151> 2002-10-09

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)...(6)

<223> C-mannosyltransferase (CMT) substrate

<223> Synthetic peptide

<400> 1

Ala Trp Ala Lys Trp Ala

1

5

<210> 2

<211> 111

<212> DNA

<213> Artificial Sequence

<220>

<221> protein\_bind

<222> (1)...(111)

<223> A forward primer carrying the signal sequence from  
eosinophil derived neurotoxin

<221> misc\_feature

<222> (19)...(79)

<223> Signal sequence from eosinophil derived neurotoxin  
(EON)

<223> Synthetic oligonucleotide

<400> 2

acagaagctt ccaccaatgg ttccaaaact gacttcccaa atttgtcttc ttctgttggg 60  
gcttctggct gtggaggggct cactccatgt ctcccctata ctaggttatt g 111

<210> 3

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<221> primer\_bind

<222> (1)...(55)

<223> A reverse primer encoding the CMT substrate site

<223> Synthetic oligonucleotide

<400> 3

atatgaattc tcagtcagtc aagcccattt agcccaagcg gatccacgcg gaacc 55

<210> 4

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<221> primer\_bind

<222> (1)...(50)

<223> Forward primer

<221> misc\_feature

<222> (14)...(19)

<223> Hind III restriction site

<221> misc\_feature

<222> (20)...(30)

<223> Kozak sequence

<223> Synthetic oligonucleotide

<400> 4

ggggtaccag atctaagctt gccaccatgg ccaagggtt ctatatttcc 50

<210> 5

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<221> protein\_bind

<222> (1)...(50)

<223> Reverse primer

<221> misc\_feature

<222> (2)...(7)

<223> Spe I sequence

<221> misc\_feature  
 <222> (8)...(29)  
 <223> A tobacco etch virus (TEV) protease site  
  
 <223> Synthetic oligonucleotide  
  
 <400> 5  
 gactagtacc ctgaaaatac aaattctcac tttgggtccaa ggtggtggcc 50  
  
 <210> 6  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> primer\_bind  
 <222> (1)...(28)  
 <223> Forward primer  
  
 <221> misc\_feature  
 <222> (2)...(7)  
 <223> Spe I restriction site  
  
 <223> Synthetic oligonucleotide  
  
 <400> 6  
 gactagttcc cctatactag gttattgg 28  
  
 <210> 7  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> primer\_bind  
 <222> (1)...(42)  
 <223> Reverse primer  
  
 <221> misc\_feature  
 <222> (9)...(14)  
 <223> Spe I restriction site  
  
 <223> Synthetic nucleotide  
  
 <400> 7  
 gctctagaga attcctatca agcccactga gcccaagcgg at 42  
  
 <210> 8  
 <211> 924  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> CDS  
 <222> (1)...(924)  
 <223> The cDNA sequence of the pSMCi-APN-GST-AWAQWA

insert

<223> Engineered sequence

<400> 8

atg gcc aag ggc ttc tat att tcc aag tcc ctg ggc atc ctg ggg atc	48
Met Ala Lys Gly Phe Tyr Ile Ser Lys Ser Leu Gly Ile Leu Gly Ile	
1 5 10 15	
ctc ctg ggc gtg gca gcc gtg tgc aca atc atc gca ctg tca gtg gtg	96
Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val	
20 25 30	
tac tcc cag gag aag aac aag aac gcc aac agc tcc ccc gtg gcc tcc	144
Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser	
35 40 45	
acc acc ccg tcc gcc tca gcc acc acc aac ccc gcc tcg gcc acc acc	192
Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr	
50 55 60	
ttg gac caa agt gag aat ttg tat ttt cag ggt act agt tcc cct ata	240
Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile	
65 70 75 80	
cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc act cga ctt ctt	288
Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu	
85 90 95	
ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg tat gag cgc gat	336
Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp	
100 105 110	
gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg ggt ttg gag ttt	384
Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe	
115 120 125	
ccc aat ctt cct tat tat att gat ggt gat gtt aaa tta aca cag tct	432
Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser	
130 135 140	
atg gcc atc ata cgt tat ata gct gac aag cac aac atg ttg ggt ggt	480
Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly	
145 150 155 160	
tgt cca aaa gag cgt gca gag att tca atg ctt gaa gga gcg gtt ttg	528
Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu	
165 170 175	
gat att aga tac ggt gtt tcg aga att gca tat agt aaa gac ttt gaa	576
Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu	
180 185 190	
act ctc aaa gtt gat ttt ctt agc aag cta cct gaa atg ctg aaa atg	624
Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met	
195 200 205	

ttc gaa gat cgt tta tgt cat aaa aca tat tta aat ggt gat cat gta	672
Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val	
210 215 220	
acc cat cct gac ttc atg ttg tat gac gct ctt gat gtt gtt tta tac	720
Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr	
225 230 235 240	
atg gac cca atg tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa	768
Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys	
245 250 255	
aaa cgt att gaa gct atc cca caa att gat aag tac ttg aaa tcc agc	816
Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser	
260 265 270	
aag tat ata gca tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt	864
Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly	
275 280 285	
ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt gga tcc gct tgg	912
Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ala Trp	
290 295 300	
gct cag tgg gct	924
Ala Gln Trp Ala	
305	

<210> 9  
 <211> 308  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Engineered sequence

<400> 9

Met Ala Lys Gly Phe Tyr Ile Ser Lys Ser Leu Gly Ile Leu Gly Ile	
1 5 10 15	
Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val	
20 25 30	
Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser	
35 40 45	
Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr	
50 55 60	
Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile	
65 70 75 80	
Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu	
85 90 95	
Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp	
100 105 110	
Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe	
115 120 125	
Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser	
130 135 140	
Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly	

145					150					155					160	
Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	
				165					170					175		
Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	
				180					185					190		
Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	
				195					200					205		
Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	
				210					215					220		
Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	
225					230					235					240	
Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	Val	Cys	Phe	Lys	
				245					250					255		
Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	Leu	Lys	Ser	Ser	
				260					265					270		
Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	
				275					280					285		
Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	Gly	Ser	Ala	Trp	
				290					295					300		
Ala	Gln	Trp	Ala													
305																